

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/236,208*TEAM 2#8
DATE: 01/05/96
TIME: 15:16:30

INPUT SET: S8120.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

*not a
sequence
case*

SEQUENCE LISTING

(1) General Information:

*See marked-up
notes*

(i) APPLICANT: Evans, Mark J.

Matis, Louis A.
Mueller, Eileen Elliott
Nye, Steven H.
Rollins, Scott
Rother, Russell P.
Springhorn, Jeremy P.
Squinto, Stephen P.
Thomas, Thomas C.
Wilkins, James A.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Seth A. Fidel
(B) STREET: 25 Science Park (Alexion)
(C) CITY: New Haven
(D) STATE: Connecticut
(E) COUNTRY: USA
(F) ZIP: 06511

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.4Mb storage
(B) COMPUTER: Macintosh Cetrus 610
(C) OPERATING SYSTEM: System 7
(D) SOFTWARE: WordPerfect 3.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/487,283

(B) FILING DATE: June 7, 1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/236,208

(B) FILING DATE: 02-MAY-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seth A. Fidel.

(B) REGISTRATION NUMBER: 38,449

(C) REFERENCE/DOCKET NUMBER: ALX-152.1 CIP

(ix) TELECOMMUNICATION INFORMATION:

*This disk was
submitted for
this application*

INPUT SET: S8120.raw

46 (A) TELEPHONE: (203) 776-1790
47 (B) TELEFAX: (203) 772-3655
48
49
50

ERRORED SEQUENCES FOLLOW:

place this
main heading
over subheading
(A) Description:

51 (2) INFORMATION FOR SEQ ID NO:1:
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 21 amino acids
54 (B) TYPE: Amino Acid
55 (C) STRANDEDNESS: Single
56 (D) TOPOLOGY: Linear
--> 57 (A) DESCRIPTION: KSSKC peptide
58 (iii) HYPOTHETICAL: No
59 (iv) ANTI-SENSE: No
60
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63 Val Ile Asp His Gln Gly Thr Lys Ser Ser
64 5 10
65
66 Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
67 15 20
68
69

(ii) Molecule Type:

70 (2) INFORMATION FOR SEQ ID NO:2:
71 (i) SEQUENCE CHARACTERISTICS:
--> 72 (A) LENGTH: 1658 Amino Acids
73 (B) TYPE: Amino Acid
74 (C) STRANDEDNESS: Single
75 (D) TOPOLOGY: Linear
--> 76 (A) DESCRIPTION: Pro-C5 Polypeptide
77 (iii) HYPOTHETICAL: No
78 (iv) ANTI-SENSE: No
79 (vi) ORIGINAL SOURCE:
80 (A) ORGANISM: Homo sapiens
81 (x) PUBLICATION INFORMATION:
82 (A) AUTHORS: Haviland, D.L.
83 Haviland, J.C.
84 Fleischer, D.T.
85 Hunt, A.
86 Wetsel, R.A.
87
88 (B) TITLE: Complete cDNA Sequence of Human
89 Complement Pro-C5
90 (C) JOURNAL: Journal of Immunology
91 (D) VOLUME: 146

include in this count the
negative numbers (1676)

(ii) Molecule Type:

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92      (F) PAGES: 362-368
93      (G) DATE: 1991
94
95
96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
97
98          Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
99              -15              -10
100
101      Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
102              -5              -1              5
103
104      Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
105              10              15              20
106
107      Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala
108              25              30
109
110      Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
111      35              40              45
112
113      Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
114      50              55              60
115
116      Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly
117      65              70              75
118
119      Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser
120      80              85              90
121
122      Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp
123      95              100
124
125      Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr
126      105              110              115
127
128      Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp
129      120              125              130
130
131      Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile
132      135              140              145
133
134      Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp
135      150              155              160
136
137      His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser
138      165              170
139
140      Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys
141      175              180              185
142
143      Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys
144      190              195              200

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145
146  Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu
147          205                      210                      215
148
149  Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile
150          220                      225                      230
151
152  Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu
153          235                      240
154
155  Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys
156  245                      250                      255
157
158  Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
159  260                      265                      270
160
161  Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu
162          275                      280                      285
163
164  Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu
165          290                      295                      300
166
167  Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser
168          305                      310
169
170  Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys
171  315                      320                      325
172
173  Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro
174  330                      335                      340
175
176  Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln
177          345                      350                      355
178
179  Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val
180          360                      365                      370
181
182  Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser
183          375                      380
184
185  Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly
186  385                      390                      395
187
188  Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val
189  400                      405                      410
190
191  Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu
192          415                      420                      425
193
194  Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser
195          430                      435                      440
196
197  Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn

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198                               445                               450
199
200  His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val
201  455                               460                               465
202
203  Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn
204  470                               475                               480
205
206  Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr
207  485                               490                               495
208
209  Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile
210  500                               505                               510
211
212  Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val
213  515                               520
214
215  Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser
216  525                               530                               535
217
218  Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln
219  540                               545                               550
220
221  Leu Gln Val His Leu Ser Pro Asp Ala Asp Ala Tyr Ser Pro
222  555                               560                               565
223
224  Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser
225  570                               575                               580
226
227  Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val
228  585                               590
229
230  Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe
231  595                               600                               605
232
233  Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Gly Leu
234  610                               615                               620
235
236  Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu
237  625                               630                               635
238
239  Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro
240  640                               645                               650
241
242  Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys
243  655                               660
244
245  Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys
246  665                               670                               675
247
248  Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr
249  680                               685                               690
250

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251  Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys
252          695                      700                      705
253
254  Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu
255          710                      715                      720
256
257  Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu
258          725                      730
259
260  His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg
261  735                      740                      745
262
263  Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val
264  750                      755                      760
265
266  Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu
267          765                      770                      775
268
269  Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly
270          780                      785                      790
271
272  Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp
273          795                      800
274
275  Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly
276  805                      810                      815
277
278  Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr
279  820                      825                      830
280
281  Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly
282          835                      840                      845
283
284  Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr
285          850                      855                      860
286
287
288  Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
289          865                      870
290
291  Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly
292  875                      880                      885
293
294  Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys
295  890                      895                      900
296
297  Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val
298          905                      910                      915
299
300  Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly
301          920                      925                      930
302
303  Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg

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304          935          940
305
306 Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile
307 945          950          955
308
309 Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile Leu Ser Ala
310 960          965          970
311
312 Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro
313 975          980          985
314
315 Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val
316 990          995          1000
317
318 Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn
319 1005          1010
320
321 Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys
322 1015          1020          1025
323
324 Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg
325 1030          1035          1040
326
327 Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala
328 1045          1050          1055
329
330 Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
331 1060          1065          1070
332
333 Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn
334 1075          1080
335
336 Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly
337 1085          1090          1095
338
339 Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln
340 1100          1105          1110
341
342 Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu
343 1115          1120          1125
344
345 Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile
346 1130          1135          1140
347
348 Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp
349 1145          1150
350
351 Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe
352 1155          1160          1165
353
354 Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
355 1170          1175          1180
356

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